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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/441,313A

DATE: 06/04/2002

TIME: 14:46:21

Input Set : A:\5709 new seq list.ST25.txt

Output Set: N:\CRF3\06042002\I441313A.raw

P.6

OK

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3 <110> APPLICANT: Svendsen, Allan
 4 Kjaerulff, Soren
 5 Bisgard-Frantzen, Henrik
 6 Andersen, Carsten
 8 <120> TITLE OF INVENTION: Alpha-amylase variants
 10 <130> FILE REFERENCE: 5709.200-US
 12 <140> CURRENT APPLICATION NUMBER: US/09/441,313A
 12 <141> CURRENT FILING DATE: 1999-11-16
 12 <160> NUMBER OF SEQ ID NOS: 31
 14 <170> SOFTWARE: PatentIn version 3.1
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 485
 18 <212> TYPE: PRT
 19 <213> ORGANISM: Bacillus sp.
 21 <400> SEQUENCE: 1
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 24 1 5 10 15
 27 Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala
 28 20 25 30
 31 Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp
 32 35 40 45
 35 Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
 36 50 55 60
 39 Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
 40 65 70 75 80
 43 Thr Arg Asn Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly
 44 85 90 95
 47 Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
 48 100 105 110
 51 Gly Thr Glu Ile Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn
 52 115 120 125
 55 Gln Glu Thr Ser Gly Glu Tyr Ala Ile Glu Ala Trp Thr Lys Phe Asp
 56 130 135 140
 59 Phe Pro Gly Arg Gly Asn Asn His Ser Ser Phe Lys Trp Arg Trp Tyr
 60 145 150 155 160
 63 His Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Gln Leu Gln Asn Lys
 64 165 170 175
 67 Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp
 68 180 185 190
 71 Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met
 72 195 200 205
 75 Asp His Pro Glu Val Ile His Glu Leu Arg Asn Trp Gly Val Trp Tyr
 76 210 215 220

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79 Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
80 225                230                235                240
83 Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr
84                245                250                255
87 Thr Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
88                260                265                270
91 Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His Ser Val
92                275                280                285
95 Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly
96                290                295                300
99 Gly Tyr Tyr Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gln Lys
100 305                310                315                320
103 His Pro Thr His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
104                325                330                335
107 Gly Glu Ala Leu Glu Ser Phe Val Gln Gln Trp Phe Lys Pro Leu Ala
108                340                345                350
111 Tyr Ala Leu Val Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
112                355                360                365
115 Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser
116                370                375                380
119 Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr Gly Thr
120 385                390                395                400
123 Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu
124                405                410                415
127 Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
128                420                425                430
131 Gly Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys Asn Lys Ala Gly
132                435                440                445
135 Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile
136                450                455                460
139 Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser
140 465                470                475                480
143 Val Trp Val Lys Gln
144                485
147 <210> SEQ ID NO: 2
148 <211> LENGTH: 485
149 <212> TYPE: PRT
150 <213> ORGANISM: Bacillus sp.
152 <400> SEQUENCE: 2
154 His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp His
155 1                5                10                15
158 Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ser
159                20                25                30
162 Asn Leu Arg Asn Arg Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Trp
163                35                40                45
166 Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
167                50                55                60
170 Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
171 65                70                75                80

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174 Thr Arg Ser Gln Leu Glu Ser Ala Ile His Ala Leu Lys Asn Asn Gly
175      85      90      95
178 Val Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
179      100      105      110
182 Ala Thr Glu Asn Val Leu Ala Val Glu Val Asn Pro Asn Asn Arg Asn
183      115      120      125
186 Gln Glu Ile Ser Gly Asp Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp
187      130      135      140
190 Phe Pro Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp Arg Trp Tyr
191 145      150      155      160
194 His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Gln Phe Gln Asn Arg
195      165      170      175
198 Ile Tyr Lys Phe Arg Gly Asp Gly Lys Ala Trp Asp Trp Glu Val Asp
199      180      185      190
202 Ser Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met
203      195      200      205
206 Asp His Pro Glu Val Val Asn Glu Leu Arg Arg Trp Gly Glu Trp Tyr
207      210      215      220
210 Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
211 225      230      235      240
214 Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Ala
215      245      250      255
218 Thr Gly Lys Glu Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
219      260      265      270
222 Gly Ala Leu Glu Asn Tyr Leu Asn Lys Thr Asn Trp Asn His Ser Val
223      275      280      285
226 Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly
227      290      295      300
230 Gly Asn Tyr Asp Met Ala Lys Leu Leu Asn Gly Thr Val Val Gln Lys
231 305      310      315      320
234 His Pro Met His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
235      325      330      335
238 Gly Glu Ser Leu Glu Ser Phe Val Gln Glu Trp Phe Lys Pro Leu Ala
239      340      345      350
242 Tyr Ala Leu Ile Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
243      355      360      365
246 Gly Asp Tyr Tyr Gly Ile Pro Thr His Ser Val Pro Ala Met Lys Ala
247      370      375      380
250 Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Asn Phe Ala Tyr Gly Thr
251 385      390      395      400
254 Gln His Asp Tyr Phe Asp His His Asn Ile Ile Gly Trp Thr Arg Glu
255      405      410      415
258 Gly Asn Thr Thr His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
259      420      425      430
262 Gly Pro Gly Gly Glu Lys Trp Met Tyr Val Gly Gln Asn Lys Ala Gly
263      435      440      445
266 Gln Val Trp His Asp Ile Thr Gly Asn Lys Pro Gly Thr Val Thr Ile
267      450      455      460
270 Asn Ala Asp Gly Trp Ala Asn Phe Ser Val Asn Gly Gly Ser Val Ser

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271 465          470          475          480
274 Ile Trp Val Lys Arg
275          485
278 <210> SEQ ID NO: 3
279 <211> LENGTH: 514
280 <212> TYPE: PRT
281 <213> ORGANISM: Bacillus stearothermophilus
283 <400> SEQUENCE: 3
285 Ala Ala Pro Phe Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr Leu
286 1          5          10          15
289 Pro Asp Asp Gly Thr Leu Trp Thr Lys Val Ala Asn Glu Ala Asn Asn
290          20          25          30
293 Leu Ser Ser Leu Gly Ile Thr Ala Leu Trp Leu Pro Pro Ala Tyr Lys
294          35          40          45
297 Gly Thr Ser Arg Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu Tyr Asp
298          50          55          60
301 Leu Gly Glu Phe Asn Gln Lys Gly Ala Val Arg Thr Lys Tyr Gly Thr
302 65          70          75          80
305 Lys Ala Gln Tyr Leu Gln Ala Ile Gln Ala Ala His Ala Ala Gly Met
306          85          90          95
309 Gln Val Tyr Ala Asp Val Val Phe Asp His Lys Gly Gly Ala Asp Gly
310          100         105         110
313 Thr Glu Trp Val Asp Ala Val Glu Val Asn Pro Ser Asp Arg Asn Gln
314          115         120         125
317 Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe Asp Phe
318          130         135         140
321 Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp Tyr His
322 145          150         155         160
325 Phe Asp Gly Val Asp Trp Asp Glu Ser Arg Lys Leu Ser Arg Ile Tyr
326          165         170         175
329 Lys Phe Arg Gly Ile Gly Lys Ala Trp Asp Trp Glu Val Asp Thr Glu
330          180         185         190
333 Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Leu Asp Met Asp His
334          195         200         205
337 Pro Glu Val Val Thr Glu Leu Lys Ser Trp Gly Lys Trp Tyr Val Asn
338          210         215         220
341 Thr Thr Asn Ile Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys
342 225          230         235         240
345 Phe Ser Phe Phe Pro Asp Trp Leu Ser Asp Val Arg Ser Gln Thr Gly
346          245         250         255
349 Lys Pro Leu Phe Thr Val Gly Glu Tyr Trp Ser Tyr Asp Ile Asn Lys
350          260         265         270
353 Leu His Asn Tyr Ile Met Lys Thr Asn Gly Thr Met Ser Leu Phe Asp
354          275         280         285
357 Ala Pro Leu His Asn Lys Phe Tyr Thr Ala Ser Lys Ser Gly Gly Thr
358          290         295         300
361 Phe Asp Met Arg Thr Leu Met Thr Asn Thr Leu Met Lys Asp Gln Pro
362 305          310         315         320
365 Thr Leu Ala Val Thr Phe Val Asp Asn His Asp Thr Glu Pro Gly Gln

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366          325          330          335
369 Ala Leu Gln Ser Trp Val Asp Pro Trp Phe Lys Pro Leu Ala Tyr Ala
370          340          345          350
373 Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr Gly Asp
374          355          360          365
377 Tyr Tyr Gly Ile Pro Gln Tyr Asn Ile Pro Ser Leu Lys Ser Lys Ile
378          370          375          380
381 Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr Gln His
382 385          390          395          400
385 Asp Tyr Leu Asp His Ser Asp Ile Ile Gly Trp Thr Arg Glu Gly Val
386          405          410          415
389 Thr Glu Lys Pro Gly Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
390          420          425          430
393 Gly Gly Ser Lys Trp Met Tyr Val Gly Lys Gln His Ala Gly Lys Val
394          435          440          445
397 Phe Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile Asn Ser
398          450          455          460
401 Asp Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser Val Trp
402 465          470          475          480
405 Val Pro Arg Lys Thr Thr Val Ser Thr Ile Ala Trp Ser Ile Thr Thr
406          485          490          495
409 Arg Pro Trp Thr Asp Glu Phe Val Arg Trp Thr Glu Pro Arg Leu Val
410          500          505          510
413 Ala Trp
417 <210> SEQ ID NO: 4
418 <211> LENGTH: 483
419 <212> TYPE: PRT
420 <213> ORGANISM: Bacillus licheniformis
422 <400> SEQUENCE: 4
424 Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro
425 1          5          10          15
428 Asn Asp Gly Gln His Trp Arg Arg Leu Gln Asn Asp Ser Ala Tyr Leu
429          20          25          30
432 Ala Glu His Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly
433          35          40          45
436 Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
437          50          55          60
440 Gly Glu Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
441 65          70          75          80
444 Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn
445          85          90          95
448 Val Tyr Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr
449          100          105          110
452 Glu Asp Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val
453          115          120          125
456 Ile Ser Gly Glu His Leu Ile Lys Ala Trp Thr His Phe His Phe Pro
457          130          135          140
460 Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe
461 145          150          155          160

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/441,313A

DATE: 06/04/2002
TIME: 14:46:22

Input Set : A:\5709 new seq list.ST25.txt
Output Set: N:\CRF3\06042002\I441313A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:15; N Pos. 21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40
Seq#:15; N Pos. 41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60
Seq#:15; N Pos. 61,62
Seq#:16; N Pos. 63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82
Seq#:16; N Pos. 83,84,85,86,87,88,89,90,91,92,93,94,95,96,97,98,99,100,101
Seq#:16; N Pos. 102,103,104
Seq#:17; N Pos. 19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38
Seq#:17; N Pos. 39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58
Seq#:17; N Pos. 59,60
Seq#:19; N Pos. 19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38
Seq#:19; N Pos. 39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58
Seq#:19; N Pos. 59,60
Seq#:21; N Pos. 54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73
Seq#:21; N Pos. 74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93
Seq#:21; N Pos. 94,95
Seq#:23; N Pos. 21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40
Seq#:23; N Pos. 41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60
Seq#:23; N Pos. 61,62

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